

DR P-PSDB; ABG04224.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity

XX Claim 1: SEQ ID NO 4215; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1137 BP; 265 A; 255 C; 260 G; 356 T; 1 other;

Query Match 2.8%; Score 81; DB 23; Length 1137;
Best Local Similarity 74.5%; Pred. No. 7.4e-12;
Matches 102; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 651 TGGTGGCCCTGGAGTACTAGTGGAGCGTGGAGTCCGGGTCAGCTCTGTACCAAGGC 710
DB 699 TAGCGCTCTGGTGAACACTCAGCGAGCGAGTGGAGTCTCGGGTTCAGCTCTGCACCAAGTC 758
QY 711 CGGCCCTGGTGCACAACTCAGGAACCTCCCTGATCTGGATGGAGCGGTGTTTCTAAGA 770
DB 759 CAGTCTGGCCAGCACTCAAGATCTCTGCTGACCAAGCGTGGAGGCTGTTGTTCTGAGA 818
QY 771 GCATCTCTAGCTGTGT 787
DB 819 ACATCTCTTCCCGCGT 835

RESULT 6

AAQ61233/c
ID AAQ61233 standard; DNA; 315 BP.

XX AAQ61233;

DT 16-MAR-1994 (first entry)

DE Human brain Expressed Sequence Tag EST01263.

KW Gene transcription product; genetic markers; tagging; in vivo;
KW transcription; mapping; locations; chromosomes; chromosomal; ss.

OS Homo sapiens.

XX W09316178-A.

XX 19-AUG-1993.

XX 12-FEB-1993; 93WO-US01294.

XX 12-FEB-1992; 92US-0837195.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICE.

XX Adams MD, Moreno RF, Venter CJ;

XX WPI; 1993-272882/34.

XX Enriched oligonucleotides and corresp. sequences - used as
PT markers for human genes transcribed in-vivo, facilitate tagging
PT of most human genes

XX Example 4; Page 459; 500pp; English.

XX The Expressed Sequence Tag was isolated from a human brain cDNA
CC library as part of a large set of ESTs which can be used as markers
CC for human genes transcribed in vivo. They can be used to facilitate
CC tagging of most human genes, for mapping locations of expressed genes
CC on chromosomes, for individual or forensic identification, for mapping
CC locations of disease-associated genes, for identification of tissue
CC type, and for prep. of antisense sequences, probes and constructs.
CC EST01263 has a "poor" coding probability as evaluated using the
CC coding-region prediction program CRM. See also AAQ59041-Q61440.

XX Sequence 315 BP; 113 A; 61 C; 49 G; 90 T; 2 other;

Query Match 2.0%; Score 59.8; DB 14; Length 315;
Best Local Similarity 60.1%; Pred. No. 3e-06;
Matches 175; Conservative 0; Mismatches 99; Indels 17; Gaps 4;

QY 2638 GTTAAAGAAAGTACTCTTAATTTATTCAATGTCTTCTTAATATCTCTTAAATAAATAA 2697
DB 298 GTCAAAATATGACATTCCTTCATTTCCATCTTAACTGTAATGTGAAATAA 239
QY 2698 GTTGGAAAGTCTATGAGACCGTACCT-AAGAAACCTTGACTGTATTAAAGTTATTAA 2756
DB 238 GTTGAAGAGCTTTGGGACCATCATACATGCAAAACGGTCCCTCTGTACTTAATTATTA 179
QY 2757 TGCATGC-----ATTGTGAAGCCCTTCCAGTGATGGTGGTGTGCTG 2805
DB 178 TANTCTATAAATGATACCAATCTGCCACCCCTTCCAGTGATGG-GGCAGTATGCTG 120
QY 2806 AGAAATGTAAGTTTGGCATGAG----GGGAGGGGCTGCTGTTCTATATTGTTTTG 2861
DB 119 AGGAAGTATATTTTCAGTACTGGGTGCGGGGAGGAGGATGTTTCTACATTTTATT 60
QY 2862 TTTTCTATAAAGTAAATCAGGATGATCTCTGTTTCATTTGACATGAAA 2912
DB 59 TTTTCTATAAATGCAATGGTCTGTATGCTGTTTATTGAAATTATA 9

RESULT 7

ABN85733

ID ABN85733 standard; DNA; 249487 BP.

XX ABN85733;

DT 30-SEP-2002 (first entry)

DE Mouse genomic region containing the ltrpc5 gene SEQ ID NO 3.

KW Mouse; ltrpc5; taste; cell signalling; TC-ICS; food; pharmaceutical;
KW taste cell-specific ion channel subunit; gene; ds.

OS Mus sp.

XX W0200254069-A1.

XX 11-JUL-2002.

XX 26-DEC-2001; 2001WO-US49808.

XX 29-DEC-2000; 2000US-259379P.

XX 21-DEC-2001; 2001US-0026188.